

7.0 SEQUENCE LISTING

(1) GENERAL INFORMATION:

- Sub B1*
- (i) APPLICANT: Ralph, David
An, Gang
O'Hara, Mark S.
Veltri, Robert
- (ii) TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING mRNA
PROFILES IN PERIPHERAL LEUKOCYTES
- (iii) NUMBER OF SEQUENCES: 55
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Arnold, White & Durkee
(B) STREET: P.O. Box 4433
(C) CITY: Houston
(D) STATE: Texas
(E) COUNTRY: USA
(F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE: Concurrently Herewith
(C) CLASSIFICATION: Unknown
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/041,576
(B) FILING DATE: 24-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Nakashima, Richard A.
(B) REGISTRATION NUMBER: P-42,023
(C) REFERENCE/DOCKET NUMBER: UROC:014
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (512) 418-3000
(B) TELEFAX: (512) 474-7577

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGTGAGCCCC AGGAGACAGA AGAGATATGA GGAAATTGTT AAGGAAGTCA GCACTTACAT 60
TAAGAAAATT GGCTACAACC CCGACACAGT AGCATTGTG CCAATTTCTG GTTGAATGG 120
TGACAACATG CTGGAGCCAA GTGCTAACAT GCCTTGTTTC AAGGGATGGA AAGTCACCCG 180
TAAGGATGGC AATGCCAGTG GAACCACGCT GCTTGAGGCT CTGGACTGCA TCCTACCACC 240
AACTCGTCCA ACTGACAAGC CCTTGC GCCTCTCCAA GGATGTTCTT ACAAATTGG 300
TGGTATTGGT ACTGTTCCCT GTTGGCCGA ATTGGAAAAC TGGTGTTCCT CCAAACCCCG 360
GTTATGGTGG GTTTCCTCCT CCTTGA 387

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGCGGAACA AGGGAGCGCT AAAAGGAAAT TAGGATGTCA GGTGCATAAA GGACATAATT 60
CCAAAACCTT TCCAAACCCC AAATTTATTC AAAGGAACTG AGGAGTGGAT TGAGGAGTGG 120
ACCAACACTG GCGCCAAACA CAGAAATTAT TGTAAGCTT TCTGATGGAA GAGAGCTCTG 180
TCTGGGCCCC AAGGAAAACCT GGGTGCAGAG GGTGTGGAG AAGTTTTTGA AGAGGGCTGA 240
GAATTCATAA AAAAATTCAT TCTCTGTGGT ATCCAAGAAT CAGTGAAGAT GCCAGTGAAA 300
CTTCAAGCAA ATCTACTTCA ACACTTCATG TATTGTGTGG GTCTGTTGTA GGGTTGCCAG 360
TTGTT 365

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCTTGGGCCC CAAGGAAAAC TGGGTGCAGA GGGTTGTGGA GAAGTTTTTG AAGAGGTAAG 60
TTATATATTT TTGAATTTAA AATTTGTCAT TTATCCGTGA GACATATAAT CCAAAGTCAG 120
CCTATAAATT TCTTTCTGTT GCTAAAAATC GTCATTAGGT ATCTGCCTTT TTGGTTAAAA 180
AAAAAAGGAA TAGCATCAAT AGTGAGTGTG TTGTACTCAT GACCAGAAAG ACCATACATA 240
GTTTGCCAG GAAATTCTGG GTTTAAGCTT GTGTCCTATA CTCTTAGTAA AGTTCTTTGT 300
CACTCCAGT AGTGTCTTAT GTTAGATGAT AATGTCTTTG ATCTCCCTAT TTATAGTTGA 360
GAATATAGAG CATGTCTAAC ACATGAATGT CAAAGACTAT ATTGACTTTT CAAGAACCCT 420
ACTTTCCTTC TTATTAAACA TAGCTCATCT TTATATTGTG AATTTTATTT TAGGGCTGAG 480
AATTCATAAA AAAATTCATT CTCTGTGGTA TCCAAGAATC AGTGAAGATG CCAGTGAAAC 540
TTCAAGCAAA TCTACTTCAA CACTTCATGT ATTGTGTGGG TCTGTTGTAG GGTTGCCA 598

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCCTCAGGC TGGGGCAGCA TT 22

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAGTGGAAG AGTCTCATTC GAGAT

25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGAGCTGCCT GACGGCCAGG TCATC

25

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGCATTG CGGTGGACGA TGGAG

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACAACATGC TGGAGCCAAG TGC

23

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACCACCAATT TTGTAAGAAC ATCCT

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGCCCCAAG GAAAACT

17

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGCAACCCT ACAACAGACC

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGCCCCAAG GAAAACT

17

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGACTCACT ATAAGCAGGA

20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGACCCAGCC CCTTGAGAAA CCT

23

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCTCAGGCT GGGGCAGCAT T

21

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTCACCTTC TGAGGGTGAA CTTGC

25

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AACAAGTGGC AA

12

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCGACAAGG AG

12

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGAGCTGCCT GACGGCCAGG TCATC

25

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTGCCAAGGA GTGCTAAAGA AC

22

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGGACCCCAA GGAAACT

18

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGGCCCAAGG AAAACT

16

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AACAGCTATG ACCATCGTGG

20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACGACTCACT ATGTGGAGAA

20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTGGCCTACG GAAGATACGA CAC

23

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACAATCCGGA GGCATCAGAA ACT

23

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGCCCCGGCC TCCTCGTCCT C

21

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGCGGCGGCA GCGGTTCTC

19

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCGGCAGGCG	CGGCAAATTA	CGTTGCCGGA	GCTGAACGGC	GCGGCTGGTC	TGAAGGCAAA	60
CAAGCGAGCG	AGCGCGCGAT	AGGGGCCGAG	AGGACGCGCA	GGTGGCGGCG	TTGCCATGTC	120
GCACGGTCAC	AGCCACGGCG	GGGGTGGCTG	CCGCTGCGCC	GCCGAACGGG	AGGAGCCGCC	180
CGAGCAGCGC	GGCCTGGCCT	ACGGCCTGTA	CCTGCGCATC	GACCTGGAGC	GGCTGCAATG	240
CCTTAACGAG	AGCCGCGAGG	GCAGCGGCCG	CGGCGTCTTC	AAGCCATGGG	AGGAGCGGAC	300
CGACCGCTCC	AAGTTTATTG	AAAGTGATGC	AGATGAAGAG	CTTCTGTTTA	ATATTCCATT	360
TACGGGCAAT	GTCAAGCTCA	AAGGCATCAT	TATAATGGGA	GAGGATGATG	ACTCACACCC	420
CTCTGAGATG	AGACTGTACA	AGAATATTCC	ACAGATGTCC	TTTGATGATA	CAGAAAGGGA	480
GCCAGATCAG	ACCTTTAGTC	TGAACCGGGA	TCTTACAGGA	GAATTAGAGT	ATGCTACAAA	540
AATTTCTCGT	TTTTCAAATG	TCTATCATCT	CTCAATTCAT	ATTTCAAAAA	ACTTCGGAGC	600
AGATACGACA	AAGGTCTTTT	ATATTGGCCT	GAGAGGAGAG	TGGACTGAGC	TTCGCCGACA	660
CGAGGTGACC	ATCTGCAATT	ACGAAGCATC	TGCCAACCCA	GCAGACCATA	GGGTCCATCA	720
GGTTACCCCA	CAGACACACT	TTATTTCTTA	AGGGCTGGCC	AAGGCTCCCA	TAGAGGCGCT	780
GTGTCAGTGA	AGATGTACGA	CTACCTGTTG	GGAAGGACAA	AGGGATGAGG	CTCCAGAGAG	840
AGTTGGCTGC	CACAGCTCTG	CCAAGCTTTG	TCTTTGGGGC	TTGCTGCAGA	AACCTGGCCT	900
ACGGAAGATA	CGACACCACT	GGGAGGGTTG	TGTAGGTGCC	AGGGGACCAT	CGTGGTTCTC	960
TAGGGCGCTG	TGGAATTGG	GTCTTGGGCT	GGGTGGCATC	TGGCAGTCAT	GGGTAACACT	1020
TGCTTTTCCA	GTTAATGTGG	CCATGTGATT	CCAAGTGTC	TGTTGCTTTG	TGGAAGATTG	1080
TTGTGTGACT	TGTTTTTTTT	ATTTTGTATT	TGTTTTTTTA	AAGGAACTA	TTTGTGGGCT	1140
ATAGGAACT	TTCTGATGCC	TCCGGATTGT	GTTAGTAGTA	GCCATCAGGA	GGGTCTCCAA	1200
CTAAACACT	TGTTCCCTGCT	TGCTCCTTTC	CCCTCTCATT	GTTCAGCATT	CTTGTCAGT	1260
TGCCCAGCTT	GGAGTTGTCT	GTCACGCACA	TGTGTCCTGT	GGTTATAGCT	AGAAGGACAG	1320

GAGTCTCCTG CTGATGCGTG ATAGCTTAAG CTTGGGGAGA AGGTCTTTTC CACTGCCTAG	1380
CTAAGCAGTC TGGGGAGAGC ATGGGGATCA TTTCTATGTG TGTGGGTAAT CTGGTCAGTA	1440
AGATTGAGAC TTAGTTAAGA TTCCCCTTGG AAATTCCTTA ATGTTTATTA GCTTCTAACT	1500
AGTGTGTAA GTCCGATGCC AGAATTTGGA GATTTGAGTT CTTCTTTTCA TGGCTTTTAT	1560
TCACTGTGAC TAATAAGCTT CCTAATAAAT CTTGCCAGA CTTAAAAAAA AAAA	1614

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTTCAAGCCG TGGGAGGACG GACCGACCGC TCCAAGTTCG CTGAAAGTGA TGC GGACGAA	60
GAGCTCCTGT TTAATATTCC GTTTACGTGC AATGTCAAGC TGAAAGGCGT CATCATAATG	120
GGCGAGGATG ATGACTCGCA CCCCTCGGAG ATGAGACTGT ACAAGAACAT TCCACAGATG	180
TCATTTGATG ACACAGAAAG GGAGCCAGAG CAGACCTTCA GTCTGAACCG AGACATTACA	240
GGAGAATTAG AATATGCTAC GAAAATCTCC AGGTTTTCAA ATGTCTATCA TCTTTCCATT	300
CATATTTCAA AAAACTTTGG AGCAGATACG ACGAAGATCT TTTATATTGG CCTGCGGGGA	360
GAGTGGACTG AGCTTCGCCG GCATGAGGTG ACCATCTGCA ACTATGAAGC GTCAGCCAAC	420
CCAGCAGACC ACCGGGTGCA TCAGGTCACC CCGCAGACAC ACTTCATTTC TTAAGGGCCA	480
GCCGGGGCTC CCTCAGATGC GCTGTTAGTG AAGATGTGCG ACCACCTGCT GCGAAGGACA	540
GAGGATGCTC CAGCAATAGT TGCCTGCCAG AGCTTTGGCC AGGCTTTGTC TCGGGGTTGC	600
TGCAGGAACC TGGCCTGTGG AAACCGCCTC ACCACCAGGA GCGGTATGGG TGCCAAGGGA	660
TAGTCTCTCT CTAAGGCACT GCAGAACTG GGTCTTAGGC TGGGTGGCAT CTGTCAGTCA	720
TGAATAATGC TCACTTCCCA GTCTGTGGCC ACGGGATCCC ATGTGTCCTT TTGCTTGATT	780
TCTTGTGTGG TTTGTCCTTT TGTGGCATCA AAAAGGATGC TTCCTTGACC GTAGAATCCT	840
TCTGAAACCC GAGTTTCGTG TTTGAATTAG CCATCAGGAG GGTCTCCAGC TAGAAACACT	900
TCGTCCCTGC TTGCTCCTCC TCCTGTCATT GCTCAGCATT CGTGTGAGG TGCCTAGCTG	960
GTGTCACATA TCAGACACAA GTGTCCCACA ATGGTGTTG GAAAGGAAGG AGTCTCCTGA	1020

TACATGACTG CTTGGGGAAG GCTTACACAG TCTAGCCAAA TTAGTTGCGA GTCCTTTCCC 1080
TGTGTGGGTG ACCTGGTTGG GGTAAACTG AGACAGTAAA GATTCCTCTT GGGACCTCCT 1140
TGGTGTTCCT CTGCTTCTAA CTCATGTTAT AAACCCAGGG CTGGAGTCTG GAGACCCTGC 1200
TCCTTCTGTT CATGGCTTTC ATTCATGGTG ACTAATGAGC TTCCTAATAA ATCCTTAGAG 1260
ACTTAAAA 1268

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Ser	His	Gly	His	Ser	His	Gly	Gly	Gly	Gly	Cys	Arg	Cys	Ala	Ala	1	5	10	15
Glu	Arg	Glu	Glu	Pro	Pro	Glu	Gln	Arg	Gly	Leu	Ala	Tyr	Gly	Leu	Tyr	20	25	30	
Leu	Arg	Ile	Asp	Leu	Glu	Arg	Leu	Gln	Cys	Leu	Asn	Glu	Ser	Arg	Glu	35	40	45	
Gly	Ser	Gly	Arg	Gly	Val	Phe	Lys	Pro	Trp	Glu	Glu	Arg	Thr	Asp	Arg	50	55	60	
Ser	Lys	Phe	Ile	Glu	Ser	Asp	Ala	Asp	Glu	Glu	Leu	Leu	Phe	Asn	Ile	65	70	75	80
Pro	Phe	Thr	Gly	Asn	Val	Lys	Leu	Lys	Gly	Ile	Ile	Ile	Met	Gly	Glu	85	90	95	
Asp	Asp	Asp	Ser	His	Pro	Ser	Glu	Met	Arg	Leu	Tyr	Lys	Asn	Ile	Pro	100	105	110	
Gln	Met	Ser	Phe	Asp	Asp	Thr	Glu	Arg	Glu	Pro	Asp	Gln	Thr	Phe	Ser	115	120	125	
Leu	Asn	Arg	Asp	Leu	Thr	Gly	Glu	Leu	Glu	Tyr	Ala	Thr	Lys	Ile	Ser	130	135	140	
Arg	Phe	Ser	Asn	Val	Tyr	His	Leu	Ser	Ile	His	Ile	Ser	Lys	Asn	Phe	145	150	155	160
Gly	Ala	Asp	Thr	Thr	Lys	Val	Phe	Tyr	Ile	Gly	Leu	Arg	Gly	Glu	Trp	165	170	175	

Thr Glu Leu Arg Arg His Glu Val Thr Ile Cys Asn Tyr Glu Ala Ser
180 185 190

Ala Asn Pro Ala Asp His Arg Val His Gln Val Thr Pro Gln Thr His
195 200 205

Phe Ile Ser
210

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Phe Lys Pro Trp Glu Glu Arg Thr Asp Arg Ser Lys Phe Ala Glu Ser
1 5 10 15

Asp Ala Asp Glu Glu Leu Leu Phe Asn Ile Pro Phe Thr Cys Asn Val
20 25 30

Lys Leu Lys Gly Val Ile Ile Met Gly Glu Asp Asp Asp Ser His Pro
35 40 45

Ser Glu Met Arg Leu Tyr Lys Asn Ile Pro Gln Met Ser Phe Asp Asp
50 55 60

Thr Glu Arg Glu Pro Glu Gln Thr Phe Ser Leu Asn Arg Asp Ile Thr
65 70 75 80

Gly Glu Leu Glu Tyr Ala Thr Lys Ile Ser Arg Phe Ser Asn Val Tyr
85 90 95

His Leu Ser Ile His Ile Ser Lys Asn Phe Gly Ala Asp Thr Thr Lys
100 105 110

Ile Phe Tyr Ile Gly Leu Arg Gly Glu Trp Thr Glu Leu Arg Arg His
115 120 125

Glu Val Thr Ile Cys Asn Tyr Glu Ala Ser Ala Asn Pro Ala Asp His
130 135 140

Arg Val His Gln Val Thr Pro Gln Thr His Phe Ile Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Cys Ser His Gly His Ser His Asn Cys Ala Ala Glu His Ile Pro Glu
1 5 10 15
Val Pro Gly Asp Asp Val Tyr Arg Tyr Asp Met Val Ser Tyr Ile Asp
20 25 30
Met Glu Lys Val Thr Thr Leu Asn Glu Ser Val Asp Gly Ala Gly Lys
35 40 45
Lys Val Phe Lys Val Met Glu Lys Arg Asp Asp Arg Leu Glu Tyr Val
50 55 60
Glu Ser Asp Cys Asp His Glu Leu Leu Phe Asn Ile Pro Phe Thr Gly
65 70 75 80
His Val Arg Leu Thr Gly Leu Ser Ile Ile Gly Asp Glu Asp Gly Ser
85 90 95
His Pro Ala Lys Ile Arg Leu Phe Lys Asp Arg Glu Ala Met Ser Phe
100 105 110
Asp Asp Cys Ser Ile Glu Ala Asp Gln Glu Ile Asp Leu Lys Gln Asp
115 120 125
Pro Gln Gly Leu Val Asp Tyr Pro Leu Lys Ala Ser Lys Phe Gly Asn
130 135 140
Ile His Asn Leu Ser Ile Leu Val Asp Ala Asn Phe Gly Glu Asp Glu
145 150 155 160
Thr Lys Ile Tyr Tyr Ile Gly Leu Arg Gly Glu Phe Gln His Glu Phe
165 170 175
Arg Gln Arg Ile Ala Ile Ala Thr Tyr Glu Ser Arg Ala Gln Leu Lys
180 185 190
Asp His Lys Asn Glu Ile Pro Asp Ala Val Ala Lys Gly Leu Phe
195 200 205

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGACTCGTCG CCATTCCCGG AGCAGGTCGG CCTCGGCCCA GGGGCGAGTA TCCGTTGCTG	60
TGTCGGAGAC ACTAGTCCCC GACACCGAGA CAGCCAGCCC TCTCCCCTGC CTCGCGGCGG	120
GAGAGCGTGT CCGGCCGGCC GGCCGGCGGG GCTCGCGCAA CCTCCCTCGC CTCCCCTTCC	180
CCCGCAGCCT CCGCCCCGCC AGGCCCGGCC CGGACTCCCG AGCCCCGGCC TCCTCGTCTT	240
CGGTCGCCGC TGCCGCCGGG CTTAACAGCC CCGTCCGCCG CTTCTCTTCC TAGTTTGAGA	300
AGCCAAGGAA GGAAACAGGG AAAAATGTCG CCATGAAGGC CGAGAACCGC TGCCGCCGCC	360
GACCCCCGCC GGCCCTGAAC GCCATGAGCC TGGGTCCCCG CCGCGCCCCG TCCGCTCCGA	420
CTGCCGTCGC CGCCGAGGCC CCCGTTGATG CCGCTGAGCT CCCCCAACGC CGCCGCCACC	480
GCCTCCGACA TGGACAAGAA CAGCGGCTCC AACAGCTCCT CCGCCTCTTC GGGCAGCAGC	540
AAAGGGCAAC AGCCGCCCCG CTCCGCCTCG GCGGGGCCAG CCGGCGAGTC TAAACCCAAG	600
AGCGAATTAC TAATTTGAGC TGGATTCAAT TTGTTGTCAG TTGATTCTGT AGTAAGGCCA	660
TATGTTGCCC CTCTGGAGGT GCTTGTC AAC TACTCTGGAT GATGGATGGA AAGAACTCCA	720
GTGGATCCAA GCGTTATAAT CGCAAACGTG AACTTTCCTA CCCC AAAAAT GAAAGTTTTA	780
ACAACCAGTC CCGTCGCTCC AGTTCACAGA AAAGCAAGAC TTTTAACAAG ATGCCTCCTC	840
AAAGGGGCGG CGGCAGCAGC AACTCTTTA GCTCTTCTTT TAATGGTGGA AGACGAGATG	900
AGGTAGCAGA GGCTCAACGG GCAGAGTTTA GCCCTGCCCA GTTCTCTGGT CCTAAGAAGA	960
TCAACCTGAA CCACTTGTTG AATTTCACTT TTGAACCCCG TGGCCAGACG GGTCACTTTG	1020
AAGGCAGTGG ACATGGTAGC TGGGGAAAGA GGAACAAGTG GGGACATAAG CCTTTTAACA	1080
AGGAACTCTT TTTACAGGCC AACTGCCAAT TTGTGGTGTC TGAAGACCAA GACTACACAG	1140
CTCATTTTGC TGATCCTGAT ACATTAGTTA ACTGGGACTT TGTGGAACAA GTGCGCATTT	1200
GTAGCCATGA AGTGCCATCT TGCCCAATAT GCCTCTATCC ACCTACTGCA GCCAAGATAA	1260
CCCGTTGTGG ACACATCTTC TGCTGGGCAT GCATCCTGCA CTATCTTTCA CTGAGTGAGA	1320

AGACGTGGAG TAAATGTCCC ATCTGTTACA GTTCTGTGCA TAAGAAGGAT CTCAAGAGTG	1380
TTGTTGCCAC AGAGTCACAT CAGTATGTTG TTGGTGATAC CATTACGATG CAGCTGATGA	1440
AGAGGGAGAA AGGGGTGTTG GTGGCTTTGC CCAAATCCAA ATGGATGAAT GTAGACCATC	1500
CCATTCATCT AGGAGATGAA CAGCACAGCC AGTACTCCAA GTTGCTGCTG GCCTCTAAGG	1560
AGCAGGTGCT GCACCGGGTA GTTCTGGAGG AGAAAGTAGC ACTAGAGCAG CAGCTGGCAG	1620
AGGAGAAGCA CACTCCCGAG TCCTGCTTTA TTGAGGCAGC TATCCAGGAG CTCAAGACTC	1680
GGGAAGAGGC TCTGTCGGGA TTGGCCGGAA GCAGAAGGGA GGTCACCTGGT GTTGTGGCTG	1740
CTCTGGAACA ACTGGTGCTG ATGGCTCCCT TGGCGAAGGA GTCTGTTTTT CAACCCAGGA	1800
AGGGTGTGCT GGAGTATCTG TCTGCCTTCG ATGAAGAAAC CACGGAAGTT TGTTCTCTGG	1860
ACACTCCTTC TAGACCTCTT GCTCTCCCTC TGGTAGAAGA GGAGGAAGCA GTGTCTGAAC	1920
CAGAGCCTGA GGGGTTGCCA GAGGCCTGTG ATGACTTGGA GTTAGCAGAT GACAATCTTA	1980
AAGAGGGGAC CATTTGCACT GAGTCCAGCC AGCAGGAACC CATCACCAAG TCAGGCTTCA	2040
CACGCCTCAG CAGCTCTCCT TGTTACTACT TTTACCAAGC GGAAGATGGA CAGCATATGT	2100
TCCTGCACCC TGTGAATGTG CGCTGCCTCG TCGGGGAGTA CGGCAGCCTG GAGAGGAGCC	2160
CCGAGAAGAT CTCAGCAACT GTGGTGGAGA TTGCTGGCTA CTCCATGTCT GAGGATGTTC	2220
GACAGCGTCA CAGATATCTC TCTCACTTGC CACTCACCTG TGAGTTCAGC ATCTGTGAAC	2280
TGGCTTTGCA ACCTCCTGTG GTCTCTAAGG AAACCCTAGA GATGTTCTCA GATGACATTG	2340
AGAAGAGGAA ACGTCAGCGC CAAAAGAAGG CTCGGGAGGA ACGCCGCCGA GAGCGCAGGA	2400
TTGAGATAGA GGAGAACAAG AAACAGGGCA AGTACCCAGA AGTCCACATT CCCCTCGAGA	2460
ATCTACAGCA GTTTCCTGCC TTCAATTCTT ATACCTGCTC CTCTGATTCT GCTTTGGGTC	2520
CCACCAGCAC CGAGGGCCAT GGGGCCCTCT CCATTTCTCC TCTCAGCAGA AGTCCAGGTT	2580
CCCATGCAGA CTTTCTGCTG ACCCCTCTGT CACCCACTGC CAGTCAGGGC AGTCCCTCAT	2640
TCTGCGTTGG GAGTCTGGAA GAAGACTCTC CCTTCCCTTC CTTTGCCCAG ATGCTGAGGG	2700
TTGGAAAAGC AAAAGCAGAT GTGTGGCCCA AAAGTCTCC AAAGAAAGAT GAGAACAGCT	2760
TAGTTCCTCC TGCCCCTGTG GACAGCGACG GGGAGAGTGA TAATTCAGAC CGTGTTCTTG	2820
TGCCCAGTTT TCAAAATTCC TTCAGCCAAG CTATTGAAGC AGCCTTCATG AAAGTGGACA	2880
CACCAGCTAC TTCAGATCCC CTCTCTGAAG AGAAAGGAGG AAAGAAAAGA AAAAAACAGA	2940

AACAGAAGCT CCTGTTTCAGC ACCTCAGTCG TCCACACCAA GTGACACTAC TGGCCCAGGC 3000
TACCTTCTCC ATCTGGTTTT TGTTTTTGTT TTTTTTCCC CCATGCTTTT GTTTGGCTGC 3060
TGTAATTTTT AAGTATTTGA GTTTGAACAG ATTAGCTCTG GGGGAGGGG GTTCCACAA 3120
TGTGAGGGGG AACCAAGAAA ATTTTAAATA CAGTGTATTT TCCAGCTTCC TGTCTTTACA 3180
CCAAAATAAA GTATTGACAC AAGAG 3205

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Met	Asp	Gly	Lys	Asn	Ser	Ser	Gly	Ser	Lys	Arg	Tyr	Asn	Arg	Lys	1	5	10	15
Arg	Glu	Leu	Ser	Tyr	Pro	Lys	Asn	Glu	Ser	Phe	Asn	Asn	Gln	Ser	Arg	20	25	30	
Arg	Ser	Ser	Ser	Gln	Lys	Ser	Lys	Thr	Phe	Asn	Lys	Met	Pro	Pro	Gln	35	40	45	
Arg	Gly	Gly	Gly	Ser	Ser	Lys	Leu	Phe	Ser	Ser	Ser	Phe	Asn	Gly	Gly	50	55	60	
Arg	Arg	Asp	Glu	Val	Ala	Glu	Ala	Gln	Arg	Ala	Glu	Phe	Ser	Pro	Ala	65	70	75	80
Gln	Phe	Ser	Gly	Pro	Lys	Lys	Ile	Asn	Leu	Asn	His	Leu	Leu	Asn	Phe	85	90	95	
Thr	Phe	Glu	Pro	Arg	Gly	Gln	Thr	Gly	His	Phe	Glu	Gly	Ser	Gly	His	100	105	110	
Gly	Ser	Trp	Gly	Lys	Arg	Asn	Lys	Trp	Gly	His	Lys	Pro	Phe	Asn	Lys	115	120	125	
Glu	Leu	Phe	Leu	Gln	Ala	Asn	Cys	Gln	Phe	Val	Val	Ser	Glu	Asp	Gln	130	135	140	
Asp	Tyr	Thr	Ala	His	Phe	Ala	Asp	Pro	Asp	Thr	Leu	Val	Asn	Trp	Asp	145	150	155	160
Phe	Val	Glu	Gln	Val	Arg	Ile	Cys	Ser	His	Glu	Val	Pro	Ser	Cys	Pro	165	170	175	

Ile Cys Leu Tyr Pro Pro Thr Ala Ala Lys Ile Thr Arg Cys Gly His
 180 185 190

Ile Phe Cys Trp Ala Cys Ile Leu His Tyr Leu Ser Leu Ser Glu Lys
 195 200 205

Thr Trp Ser Lys Cys Pro Ile Cys Tyr Ser Ser Val His Lys Lys Asp
 210 215 220

Leu Lys Ser Val Val Ala Thr Glu Ser His Gln Tyr Val Val Gly Asp
 225 230 235 240

Thr Ile Thr Met Gln Leu Met Lys Arg Glu Lys Gly Val Leu Val Ala
 245 250 255

Leu Pro Lys Ser Lys Trp Met Asn Val Asp His Pro Ile His Leu Gly
 260 265 270

Asp Glu Gln His Ser Gln Tyr Ser Lys Leu Leu Leu Ala Ser Lys Glu
 275 280 285

Gln Val Leu His Arg Val Val Leu Glu Glu Lys Val Ala Leu Glu Gln
 290 295 300

Gln Leu Ala Glu Glu Lys His Thr Pro Glu Ser Cys Phe Ile Glu Ala
 305 310 315 320

Ala Ile Gln Glu Leu Lys Thr Arg Glu Glu Ala Leu Ser Gly Leu Ala
 325 330 335

Gly Ser Arg Arg Glu Val Thr Gly Val Val Ala Ala Leu Glu Gln Leu
 340 345 350

Val Leu Met Ala Pro Leu Ala Lys Glu Ser Val Phe Gln Pro Arg Lys
 355 360 365

Gly Val Leu Glu Tyr Leu Ser Ala Phe Asp Glu Glu Thr Thr Glu Val
 370 375 380

Cys Ser Leu Asp Thr Pro Ser Arg Pro Leu Ala Leu Pro Leu Val Glu
 385 390 395 400

Glu Glu Glu Ala Val Ser Glu Pro Glu Pro Glu Gly Leu Pro Glu Ala
 405 410 415

Cys Asp Asp Leu Glu Leu Ala Asp Asp Asn Leu Lys Glu Gly Thr Ile
 420 425 430

Cys Thr Glu Ser Ser Gln Gln Glu Pro Ile Thr Lys Ser Gly Phe Thr
 435 440 445

Arg Leu Ser Ser Ser Pro Cys Tyr Tyr Phe Tyr Gln Ala Glu Asp Gly
 450 455 460

Gln	His	Met	Phe	Leu	His	Pro	Val	Asn	Val	Arg	Cys	Leu	Val	Arg	Glu	465	470	475	480
Tyr	Gly	Ser	Leu	Glu	Arg	Ser	Pro	Glu	Lys	Ile	Ser	Ala	Thr	Val	Val	485	490	495	
Glu	Ile	Ala	Gly	Tyr	Ser	Met	Ser	Glu	Asp	Val	Arg	Gln	Arg	His	Arg	500	505	510	
Tyr	Leu	Ser	His	Leu	Pro	Leu	Thr	Cys	Glu	Phe	Ser	Ile	Cys	Glu	Leu	515	520	525	
Ala	Leu	Gln	Pro	Pro	Val	Val	Ser	Lys	Glu	Thr	Leu	Glu	Met	Phe	Ser	530	535	540	
Asp	Asp	Ile	Glu	Lys	Arg	Lys	Arg	Gln	Arg	Gln	Lys	Lys	Ala	Arg	Glu	545	550	555	560
Glu	Arg	Arg	Arg	Glu	Arg	Arg	Ile	Glu	Ile	Glu	Glu	Asn	Lys	Lys	Gln	565	570	575	
Gly	Lys	Tyr	Pro	Glu	Val	His	Ile	Pro	Leu	Glu	Asn	Leu	Gln	Gln	Phe	580	585	590	
Pro	Ala	Phe	Asn	Ser	Tyr	Thr	Cys	Ser	Ser	Asp	Ser	Ala	Leu	Gly	Pro	595	600	605	
Thr	Ser	Thr	Glu	Gly	His	Gly	Ala	Leu	Ser	Ile	Ser	Pro	Leu	Ser	Arg	610	615	620	
Ser	Pro	Gly	Ser	His	Ala	Asp	Phe	Leu	Leu	Thr	Pro	Leu	Ser	Pro	Thr	625	630	635	640
Ala	Ser	Gln	Gly	Ser	Pro	Ser	Phe	Cys	Val	Gly	Ser	Leu	Glu	Glu	Asp	645	650	655	
Ser	Pro	Phe	Pro	Ser	Phe	Ala	Gln	Met	Leu	Arg	Val	Gly	Lys	Ala	Lys	660	665	670	
Ala	Asp	Val	Trp	Pro	Lys	Thr	Ala	Pro	Lys	Lys	Asp	Glu	Asn	Ser	Leu	675	680	685	
Val	Pro	Pro	Ala	Pro	Val	Asp	Ser	Asp	Gly	Glu	Ser	Asp	Asn	Ser	Asp	690	695	700	
Arg	Val	Pro	Val	Pro	Ser	Phe	Gln	Asn	Ser	Phe	Ser	Gln	Ala	Ile	Glu	705	710	715	720
Ala	Ala	Phe	Met	Lys	Leu	Asp	Thr	Pro	Ala	Thr	Ser	Asp	Pro	Leu	Ser	725	730	735	
Glu	Glu	Lys	Gly	Gly	Lys	Lys	Arg	Lys	Lys	Gln	Lys	Gln	Lys	Leu	Leu	740	745	750	

Phe Ser Thr Ser Val Val His Thr Lys
755 760

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Cys Pro Ile Cys Leu Tyr Pro Pro Thr Ala Ala Lys Ile Thr Arg Cys
1 5 10 15

Gly His Ile Phe Cys Trp Ala Cys Ile Leu His Tyr Leu Ser Leu Ser
20 25 30

Glu Lys Thr Trp Ser Lys Cys Pro Ile Cys
35 40

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Cys Pro Ile Cys Leu Glu Leu Ile Lys Glu Pro Val Ser Thr Lys Cys
1 5 10 15

Asp His Ile Phe Cys Lys Phe Cys Met Leu Lys Leu Leu Asn Gln Lys
20 25 30

Lys Gly Pro Ser Gln Cys Pro Leu Cys
35 40

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Cys Pro Ile Cys Leu Glu Leu Lys Glu Pro Val Ser Ala Asp Cys
1 5 10 15
Asn His Ser Phe Cys Arg Ala Cys Ile Thr Leu Asn Tyr Glu Ser Asn
20 25 30
Arg Asn Thr Asp Gly Lys Gly Asn Cys Pro Val Cys
35 40

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Cys Ala Phe Cys His Ser Val Leu His Asn Pro His Gln Thr Gly Cys
1 5 10 15
Gly His Arg Phe Cys Gln Gln Cys Ile Arg Ser Leu Arg Glu Leu Asn
20 25 30
Ser Val Pro Ile Cys Pro Val Asp
35 40

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Cys Pro Ile Cys Met Glu Ser Phe Thr Glu Glu Gln Leu Arg Pro Lys
1 5 10 15

Leu Leu His Cys Gly His Thr Ile Cys Arg Gln Cys Leu Glu Lys Leu
20 25 30

Leu Ala Ser Ser Ile Asn Gly Val Arg Cys Pro Phe Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Cys Pro Arg Cys Lys Thr Thr Lys Tyr Arg Asn Pro Ser Leu Lys Leu
1 5 10 15

Met Val Asn Val Cys Gly His Thr Leu Cys Glu Ser Cys Val Asp Leu
20 25 30

Leu Phe Val Arg Gly Ala Gly Asn Cys Pro Glu Cys
35 40

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Cys Pro Arg Cys Lys Thr Thr Lys Tyr Arg Asn Pro Ser Leu Lys Leu
1 5 10 15

Met Val Asn Val Cys Gly His Thr Leu Cys Glu Ser Cys Val Asp Leu
20 25 30

Leu Phe Val Arg Gly Ala Gly Asn Cys Pro Glu Cys
35 40

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Cys	Val	Leu	Cys	Gly	Gly	Tyr	Phe	Ile	Asp	Ala	Thr	Thr	Ile	Ile	Glu
1			5					10					15		
Cys	Leu	His	Phe	Ser	Cys	Lys	Thr	Cys	Ile	Val	Arg	Tyr	Leu	Glu	Thr
		20					25						30		
Ser	Lys	Tyr	Cys	Pro	Ile	Cys									
		35													

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Cys	Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	Gly	Asp	Lys	Leu	Arg	Ile
1			5					10					15		
Leu	Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys	Cys	Val	Asp	Pro	Trp	Leu
		20					25						30		
Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys								
		35				40									

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Cys	Thr	Ile	Cys	Tyr	Glu	Asn	Pro	Ile	Asp	Ser	Val	Leu	Tyr	Met	Cys
1			5					10					15		

Gly His Met Cys Met Cys Tyr Asp Cys Ala Ile Glu Gln Trp Arg Gly
 20 25 30

Val Gly Gly Gly Gln Cys Pro Leu Cys
 35 40

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AACAGCTATG ACCCTGAGGA 20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAGCCCCAAG CCCAGAGACA AGAT 24

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGCAGGGGCT TGTGACTCTA AGATGGCTTC ATTCACATGC CTAGGGCCTC AGTAGGATGA 60
 CTGGCATGGC CCTGGAAAAC TGCGAAGTCT TCTCTCTGTG CAAACTTTCA CCTGGACTTT 120
 TTATATGATT CTGGAAGTAT TCCAAGAAGG CAAAAGTAAA AACTGCAAAG CGTCTTAAAA 180
 TAGAAGTTCA GAAGCCACAT TATATCACTT CTGTTGCATT CTATCAAAGC AAGTCACAAG 240
 CCCCTGCCAA TCA 253

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CACACACTCC CCCATTCTGA GCCCCAAGAG GCTCATCCCT AAGGATGTCC AGAGATCCAA 60
GTGCAGAAGG AGAATGTGGT GAGGCTATTT ATTCCCCCAG TGCCTTCCCT GCTGGGCTAT 120
GGATGAACAG TGGCTGACTT CATCTAGGAA AGAGCTATGG CTTCTGTCTC CTGGAGCTCA 180
CCA 183

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGCAAAC TTT CACCTGGACT T 21

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTGTGACTT GCTTTGATAG AATG 24

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGTCCAGAGA TCCAAGTGCA GAAGG

25

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAGCTCCAGG AGACAGAAGC CATAG

25

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACATTGAAGC ACTCCGCGAC

20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGAGTGGCAG CAACCAAGCT

20